

SEQUENCE LISTING

<110> YAMAMOTO, Kazuo
Sumitomo Corporation

<120> Carbohydrate library constructed by Gene Alteration of Cargo
Receptors

<130> PH-1716PCT

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<150> JP 2002-238559

<151> 2002-08-19

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<170> PatentIn Ver. 2.0

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<213> Homo sapiens

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<222> (22)..(1554)

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<222> (22)..(112)

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gcc	aga	gtt	cgg	ccg	ctg	ttc	tgc	gcc	ttg	ctg	ctg	tca	ctc	ggt	cgc	99
Ala	Arg	Val	Arg	Pro	Leu	Phe	Cys	Ala	Leu	Leu	Leu	Ser	Leu	Gly	Arg	
				15					20					25		

ttc	gtc	cgg	ggc	gac	ggc	gtg	gga	gga	gac	ccc	gcg	gtc	gcg	ttg	cca	147
Phe	Val	Arg	Gly	Asp	Gly	Val	Gly	Gly	Asp	Pro	Ala	Val	Ala	Leu	Pro	

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cat cgc cgt ttc gag tac aaa tac agc ttc aag ggg ccg cac ctg gtg			195
His Arg Arg Phe Glu Tyr Lys Tyr Ser Phe Lys Gly Pro His Leu Val			
45	50	55	
cag agc gac ggg acc gtg ccc ttc tgg gcc cac gcg ggg aat gct att			243
Gln Ser Asp Gly Thr Val Pro Phe Trp Ala His Ala Gly Asn Ala Ile			
60	65	70	
cca agt tca gat caa att cga gta gca cca tct tta aaa agc caa aga			291
Pro Ser Ser Asp Gln Ile Arg Val Ala Pro Ser Leu Lys Ser Gln Arg			
75	80	85	90
ggc tca gtg tgg aca aag aca aaa gcg gcc ttt gag aac tgg gaa gtt			339
Gly Ser Val Trp Thr Lys Thr Lys Ala Ala Phe Glu Asn Trp Glu Val			
95	100	105	
gag gtg aca ttt cga gtg act gga aga ggt cga att gga gct gat ggc			387
Glu Val Thr Phe Arg Val Thr Gly Arg Gly Arg Ile Gly Ala Asp Gly			
110	115	120	
cta gca att tgg tat gca gaa aat caa ggc ttg gag ggc cct gtg ttt			435
Leu Ala Ile Trp Tyr Ala Glu Asn Gln Gly Leu Glu Gly Pro Val Phe			
125	130	135	
gga tca gct gat ctg tgg aat ggt gtt gga ata ttt ttt gat act ttt			483
Gly Ser Ala Asp Leu Trp Asn Gly Val Gly Ile Phe Phe Asp Thr Phe			
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Asp Asn Asp Gly Lys Lys Asn Asn Pro Ala Ile Val Ile Ile Gly Asn			
155	160	165	170
aat gga caa atc cat tat gac cat caa aat gac ggg gct agt caa gct			579
Asn Gly Gln Ile His Tyr Asp His Gln Asn Asp Gly Ala Ser Gln Ala			
175	180	185	
ttg gca agt tgc cag agg gac ttc cgc aac aaa ccc tat cct gtc cga			627
Leu Ala Ser Cys Gln Arg Asp Phe Arg Asn Lys Pro Tyr Pro Val Arg			
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gca aag att acc tat tac cag aac aca ctg aca gta atg atc aat aat			675
Ala Lys Ile Thr Tyr Tyr Gln Asn Thr Leu Thr Val Met Ile Asn Asn			
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Gly Phe Thr Pro Asp Lys Asn Asp Tyr Glu Phe Cys Ala Lys Val Glu	
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aat atg att atc cct gca caa ggg cat ttt gga ata tct gct gca act	771
Asn Met Ile Ile Pro Ala Gln Gly His Phe Gly Ile Ser Ala Ala Thr	
235 240 245 250	
gga ggt ctt gca gat gac cat gat gtc ctt tct ttt ctg act ttc cag	819
Gly Gly Leu Ala Asp Asp His Asp Val Leu Ser Phe Leu Thr Phe Gln	
255 260 265	
ttg act gaa cct gga aaa gag ccg ccc aca cca gat aaa gaa att tcg	867
Leu Thr Glu Pro Gly Lys Glu Pro Pro Thr Pro Asp Lys Glu Ile Ser	
270 275 280	
gaa aag gaa aaa gaa aag tat cag gag gaa ttt gag cac ttt caa caa	915
Glu Lys Glu Lys Glu Lys Tyr Gln Glu Glu Phe Glu His Phe Gln Gln	
285 290 295	
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Glu Leu Asp Lys Lys Lys Glu Glu Phe Gln Lys Gly His Pro Asp Leu	
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Gln Gly Gln Pro Ala Glu Glu Ile Phe Glu Ser Val Gly Asp Arg Glu	
315 320 325 330	
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Leu Arg Gln Val Phe Glu Gly Gln Asn Arg Ile His Leu Glu Ile Lys	
335 340 345	
cag ctg aac cgg cag tta gat atg att ctt gat gaa cag aga aga tat	1107
Gln Leu Asn Arg Gln Leu Asp Met Ile Leu Asp Glu Gln Arg Arg Tyr	
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gtc tct tcc tta aca gag gaa atc tct aaa aga gga gca gga atg cct	1155
Val Ser Ser Leu Thr Glu Glu Ile Ser Lys Arg Gly Ala Gly Met Pro	
365 370 375	
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Gly Gln His Gly Gln Ile Thr Gln Gln Glu Leu Asp Thr Val Val Lys	
380 385 390	

act cag cat gag att ctg aga caa gta aat gaa atg aaa aat tcc atg 1251
Thr Gln His Glu Ile Leu Arg Gln Val Asn Glu Met Lys Asn Ser Met
395 400 405 410

gga ggc gtc tat gag aca aca cag cac ttc att gac atc aaa gag cac 1347
Gly Gly Val Tyr Glu Thr Thr Gln His Phe Ile Asp Ile Lys Glu His
430 435 440

cca tca aat gaa aag cgc aaa tgc cca gaa cta cca cca ttt cca tca 1443
Pro Ser Asn Glu Lys Pro Lys Cys Pro Glu Leu Pro Pro Phe Pro Ser
460 465 470

tta ttc att ggt tat atc atg tat agg tct cag caa gaa gca gct gcc 1539
Leu Phe Ile Gly Tyr Ile Met Tyr Arg Ser Gln Gln Glu Ala Ala Ala
495 500 505

tgagtcgttt tgagggaatt taagtattta aattgcttca tagtctaaat tattaatttt 1654

caaccacatt ttaatttggt cacagtatgt aaatctgtct aaatttcagt gaatttctgg 1774

caaccctgga tatgaatgtt accccctaag tctccaatat tgcaggtttc cctgtataac 1894

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 Val Gly Gly Asp Pro Ala Val Ala Leu Pro His Arg Arg Phe Glu Tyr
 35 40 45
 Lys Tyr Ser Phe Lys Gly Pro His Leu Val Gln Ser Asp Gly Thr Val
 50 55 60

Pro Phe Trp Ala His Ala Gly Asn Ala Ile Pro Ser Ser Asp Gln Ile
 65 70 75 80

Arg Val Ala Pro Ser Leu Lys Ser Gln Arg Gly Ser Val Trp Thr Lys
 85 90 95

Thr Lys Ala Ala Phe Glu Asn Trp Glu Val Glu Val Thr Phe Arg Val
 100 105 110

Thr Gly Arg Gly Arg Ile Gly Ala Asp Gly Leu Ala Ile Trp Tyr Ala
 115 120 125

Glu Asn Gln Gly Leu Glu Gly Pro Val Phe Gly Ser Ala Asp Leu Trp
 130 135 140

Asn Gly Val Gly Ile Phe Phe Asp Thr Phe Asp Asn Asp Gly Lys Lys
 145 150 155 160

Asn Asn Pro Ala Ile Val Ile Ile Gly Asn Asn Gly Gln Ile His Tyr
 165 170 175

Asp His Gln Asn Asp Gly Ala Ser Gln Ala Leu Ala Ser Cys Gln Arg
 180 185 190

Asp Phe Arg Asn Lys Pro Tyr Pro Val Arg Ala Lys Ile Thr Tyr Tyr
 195 200 205

Gln Asn Thr Leu Thr Val Met Ile Asn Asn Gly Phe Thr Pro Asp Lys
 210 215 220

Asn Asp Tyr Glu Phe Cys Ala Lys Val Glu Asn Met Ile Ile Pro Ala
 225 230 235 240

Gln Gly His Phe Gly Ile Ser Ala Ala Thr Gly Gly Leu Ala Asp Asp
 245 250 255

His Asp Val Leu Ser Phe Leu Thr Phe Gln Leu Thr Glu Pro Gly Lys
 260 265 270

Glu Pro Pro Thr Pro Asp Lys Glu Ile Ser Glu Lys Glu Lys Glu Lys
 275 280 285

Tyr Gln Glu Glu Phe Glu His Phe Gln Gln Glu Leu Asp Lys Lys Lys
 290 295 300

Glu Glu Phe Gln Lys Gly His Pro Asp Leu Gln Gly Gln Pro Ala Glu
305 310 315 320

Glu Ile Phe Glu Ser Val Gly Asp Arg Glu Leu Arg Gln Val Phe Glu
325 330 335

Gly Gln Asn Arg Ile His Leu Glu Ile Lys Gln Leu Asn Arg Gln Leu
340 345 350

Asp Met Ile Leu Asp Glu Gln Arg Arg Tyr Val Ser Ser Leu Thr Glu
355 360 365

Glu Ile Ser Lys Arg Gly Ala Gly Met Pro Gly Gln His Gly Gln Ile
370 375 380

Thr Gln Gln Glu Leu Asp Thr Val Val Lys Thr Gln His Glu Ile Leu
385 390 395 400

Arg Gln Val Asn Glu Met Lys Asn Ser Met Ser Glu Thr Val Arg Leu
405 410 415

Val Ser Gly Met Gln His Pro Gly Ser Ala Gly Gly Val Tyr Glu Thr
420 425 430

Thr Gln His Phe Ile Asp Ile Lys Glu His Leu His Ile Val Lys Arg
435 440 445

Asp Ile Asp Asn Leu Val Gln Arg Asn Met Pro Ser Asn Glu Lys Pro
450 455 460

Lys Cys Pro Glu Leu Pro Pro Phe Pro Ser Cys Leu Ser Thr Val His
465 470 475 480

Phe Ile Ile Phe Val Val Val Gln Thr Val Leu Phe Ile Gly Tyr Ile
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ctg gga agg cct ggg ctt ctc ggc ccc ggc cct ggc ccc act aca cct	96
Leu Gly Arg Pro Gly Leu Leu Gly Pro Gly Pro Gly Pro Thr Thr Pro	
20 25 30	
ctc ttt ctt ctt ttg ttg ttg ggg tct gtg act gcg gat ata act gac	144
Leu Phe Leu Leu Leu Leu Leu Gly Ser Val Thr Ala Asp Ile Thr Asp	
35 40 45	
ggc aac agt gaa cat ctc aag cgg gag cat tcg ctc att aag ccc tac	192
Gly Asn Ser Glu His Leu Lys Arg Glu His Ser Leu Ile Lys Pro Tyr	
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caa ggg gtc ggt tcc agc tct atg ccc ctc tgg gac ttc cag ggc agc	240
Gln Gly Val Gly Ser Ser Ser Met Pro Leu Trp Asp Phe Gln Gly Ser	
65 70 75 80	
act atg ctc acg agc cag tac gta cgt ctg acc cct gac gag cgc agc	288
Thr Met Leu Thr Ser Gln Tyr Val Arg Leu Thr Pro Asp Glu Arg Ser	
85 90 95	
aaa gag ggc tct atc tgg aac cac cag cgg tgc ttc ctc aaa gac tgg	336
Lys Glu Gly Ser Ile Trp Asn His Gln Pro Cys Phe Leu Lys Asp Trp	
100 105 110	
gaa atg cac gtc cac ttc aaa gtc cac ggc aca ggg aag aag aac ctc	384
Glu Met His Val His Phe Lys Val His Gly Thr Gly Lys Lys Asn Leu	
115 120 125	
cat gga gac ggc atc gcc ttg tgg tac acc cgg gac cgc ctc gtg cca	432
His Gly Asp Gly Ile Ala Leu Trp Tyr Thr Arg Asp Arg Leu Val Pro	
130 135 140	
ggg cct gtg ttt gga agc aaa gat aac ttc cac ggc tta gcc atc ttc	480

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145					150					155					160	
ctg	gac	acc	tac	ccc	aat	gat	gag	acc	act	gag	cgc	gtg	ttc	ccg	tac	528
Leu	Asp	Thr	Tyr	Pro	Asn	Asp	Glu	Thr	Thr	Glu	Arg	Val	Phe	Pro	Tyr	
				165					170					175		
atc	tcg	gtg	atg	gtg	aac	aat	ggc	tcc	ctg	tcc	tac	gac	cac	agc	aag	576
Ile	Ser	Val	Met	Val	Asn	Asn	Gly	Ser	Leu	Ser	Tyr	Asp	His	Ser	Lys	
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gat	ggg	cgc	tgg	acc	gag	ctg	gcg	ggc	tgc	acg	gct	gac	ttc	cgc	aac	624
Asp	Gly	Arg	Trp	Thr	Glu	Leu	Ala	Gly	Cys	Thr	Ala	Asp	Phe	Arg	Asn	
		195					200					205				
cgc	gat	cac	gac	acc	ttc	ctg	gct	gtg	cgc	tac	tcc	cgg	ggc	cgt	ctg	672
Arg	Asp	His	Asp	Thr	Phe	Leu	Ala	Val	Arg	Tyr	Ser	Arg	Gly	Arg	Leu	
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acg	gtg	atg	acc	gac	ctg	gag	gac	aag	aac	gag	tgg	aag	aac	tgc	att	720
Thr	Val	Met	Thr	Asp	Leu	Glu	Asp	Lys	Asn	Glu	Trp	Lys	Asn	Cys	Ile	
225					230					235				240		
gac	atc	acg	gga	gtg	cgc	ctg	ccc	acc	ggc	tac	tac	ttc	ggg	gcc	tcc	768
Asp	Ile	Thr	Gly	Val	Arg	Leu	Pro	Thr	Gly	Tyr	Tyr	Phe	Gly	Ala	Ser	
			245						250					255		
gcc	ggc	acc	ggc	gac	ctg	tct	gac	aat	cat	gac	atc	atc	tcc	atg	aag	816
Ala	Gly	Thr	Gly	Asp	Leu	Ser	Asp	Asn	His	Asp	Ile	Ile	Ser	Met	Lys	
			260					265					270			
ctg	ttc	cag	ctg	atg	gtg	gag	cac	acg	ccc	gac	gag	gag	agc	atc	gac	864
Leu	Phe	Gln	Leu	Met	Val	Glu	His	Thr	Pro	Asp	Glu	Glu	Ser	Ile	Asp	
		275					280					285				
tgg	acc	aag	atc	gag	ccc	agc	gtc	aac	ttc	ctc	aag	tcg	ccc	aaa	gac	912
Trp	Thr	Lys	Ile	Glu	Pro	Ser	Val	Asn	Phe	Leu	Lys	Ser	Pro	Lys	Asp	
	290					295					300					
aac	gtg	gac	gac	ccc	acg	ggg	aac	ttc	cgc	agc	ggg	ccc	ctg	acg	ggg	960
Asn	Val	Asp	Asp	Pro	Thr	Gly	Asn	Phe	Arg	Ser	Gly	Pro	Leu	Thr	Gly	
305					310					315				320		
tgg	cgg	gtg	ttc	ctg	ctg	ctg	ctg	tgc	gct	ctc	ctg	ggc	atc	gtt	gtc	1008
Trp	Arg	Val	Phe	Leu	Leu	Leu	Leu	Cys	Ala	Leu	Leu	Gly	Ile	Val	Val	

325	330	335	
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Cys Ala Val Val Gly Ala Val Val Phe Gln Lys Arg Gln Glu Arg Asn			
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Lys Arg Phe Tyr			
355			
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Leu Phe Leu Leu Leu Leu Gly Ser Val Thr Ala Asp Ile Thr Asp			
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Gly Asn Ser Glu His Leu Lys Arg Glu His Ser Leu Ile Lys Pro Tyr			
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Gln Gly Val Gly Ser Ser Ser Met Pro Leu Trp Asp Phe Gln Gly Ser			
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Thr Met Leu Thr Ser Gln Tyr Val Arg Leu Thr Pro Asp Glu Arg Ser			
85	90	95	
Lys Glu Gly Ser Ile Trp Asn His Gln Pro Cys Phe Leu Lys Asp Trp			

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165					170					175						
Ile	Ser	Val	Met	Val	Asn	Asn	Gly	Ser	Leu	Ser	Tyr	Asp	His	Ser	Lys	
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Arg	Asp	His	Asp	Thr	Phe	Leu	Ala	Val	Arg	Tyr	Ser	Arg	Gly	Arg	Leu	
210					215					220						
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225					230					235					240	
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245					250					255						
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Trp	Arg	Val	Phe	Leu	Leu	Leu	Leu	Cys	Ala	Leu	Leu	Gly	Ile	Val	Val	
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340

345

350

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: synthetic
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<212> DNA

<213> Artificial Sequence

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27

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<211> 9

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Asp Pro Asp Ser Asn Gly Gly Ser Phe

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5